```
 1 GTTATTTCAG GCCATGGTGT TGCGCCGAAT TAATTCCCGA TCCAGACATG ATAAGATACA TTGATGAGTT TGGACAAACC ACAACTAGAA TGCAGTGAAA
   CAATAAAGTC CGGTACCACA ACGCGGCTTA ATTAAGGGCT AGGTCTGTAC TATTCTATGT AACTACTCAA ACCTGTTTGG TGTTGATCTT ACGTCACTTT
   (SEQ ID NO: 1)
101 AAAATGCTTT ATTTGTGAAA TTTGTGATGC TATTGCTTTA TTTGTAACCA TTATAAGCTG CAATAAACAA GTTGGGCCAT GGCGGCCAAG CTTCTGCAGG
   TTTTACGAAA TAAACACTTT AAACACTACG ATAACGAAAT AAACATTGGT AATATTCGAC GTTATTTGTT CAACCCGGTA CCGCCGGTTC GAAGACGTCC
201 TCGACTCTAG AGGATCCCCG GGGAATTCCG GCATGACTCG ATCGCCGCCC CTCAGAGAGC TGCCCCCGAG TTACACACCC CCAGCTCGAA CCGCAGCACC
   AGCTGAGATC TCCTAGGGGC CCCTTAAGGC CGTACTGAGC TAGCGGCGGG GAGTCTCTCG ACGGGGGCTC AATGTGTGGG GGTCGAGCTT GGCGTCGTGG
 1                                   M  T  R  S  P  P  L  R  E  L  P  P  S  Y  T  P  P  A  R  T  A  A  P
                ^insert starts here  (SEQ ID NO: 2)
301 CCAGATCCTA GCTGGGAGCC TGAAGGCTCC ACTCTGGCTT CGTGCTTACT TCCAGGGCCT GCTCTTCTCT CTGGGATGCG GGATCCAGAG ACATTGTGGC
   GGTCTAGGAT CGACCCTCGG ACTTCCGAGG TGAGACCGAA GCACGAATGA AGGTCCCGGA CGAGAAGAGA GACCCTACGC CCTAGGTCTC TGTAACACCG
 24 Q  I  L  A  G  S  L  K  A  P  L  W  L  R  A  Y  F  Q  G  L  L  F  S  L  G  C  G  I  Q  R  H  C  G
401 AAAGTGCTCT TTCTGGGACT GTTGGCCTTT GGGGCCCTGG CATTAGGTCT CCGCATGGCC ATTATTGAGA CAAACTTGGA ACAGCTCTGG GTAGAAGTGG
   TTTCACGAGA AAGACCCTGA CAACCGGAAA CCCCGGGACC GTAATCCAGA GGCGTACCGG TAATAACTCT GTTTGAACCT TGTCGAGACC CATCTTCACC
 57 K  V  L  F  L  G  L  L  A  F  G  A  L  A  L  G  L  R  M  A  I  I  E  T  N  L  E  Q  L  W  V  E  V  G
501 GCAGCCGGGT GAGCCAGGAG CTGCATTACA CCAAGGAGAA GCTGGGGGAG GAGGCTGCAT ACACCTCTCA GATGCTGATA CAGACCGCAC GCCAGGAGGG
   CGTCGGCCCA CTCGGTCCTC GACGTAATGT GGTTCCTCTT CGACCCCCTC CTCCGACGTA TGTGGAGAGT CTACGACTAT GTCTGGCGTG CGGTCCTCCC
 91  S  R  V  S  Q  E  L  H  Y  T  K  E  K  L  G  E  E  A  A  Y  T  S  Q  M  L  I  Q  T  A  R  Q  E  G
601 AGAGAACATC CTCACACCCG AAGCACTTGG CCTCCACCTC CAGGCAGCCC TCACTGCCAG TAAAGTCCAA GTATCACTCT ATGGGAAGTC CTGGGATTTG
   TCTCTTGTAG GAGTGTGGGC TTCGTGAACC GGAGGTGGAG GTCCGTCGGG AGTGACGGTC ATTTCAGGTT CATAGTGAGA TACCCTTCAG GACCCTAAAC
124 E  N  I  L  T  P  E  A  L  G  L  H  L  Q  A  A  L  T  A  S  K  V  Q  V  S  L  Y  G  K  S  W  D  L
701 AACAAAATCT GCTACAAGTC AGGAGTTCCC CTTATTGAAA ATGGAATGAT TGAGTGGATG ATTGAGAAGC TGTTTCCGTG CGTGATCCTC ACCCCCCTCG
   TTGTTTTAGA CGATGTTCAG TCCTCAAGGG GAATAACTTT TACCTTACTA ACTCACCTAC TAACTCTTCG ACAAAGGCAC GCACTAGGAG TGGGGGGAGC
157 N  K  I  C  Y  K  S  G  V  P  L  I  E  N  G  M  I  E  W  M  I  E  K  L  F  P  C  V  I  L  T  P  L  D
801 ACTGCTTCTG GGAGGGAGCC AAACTCCAAG GGGGCTCCGC CTACCTGCCC GGCCGCCCGG ATATCCAGTG GACCAACCTG GATCCAGAGC AGCTGCTGGA
   TGACGAAGAC CCTCCCTCGG TTTGAGGTTC CCCCGAGGCG GATGGACGGG CCGGCGGGCC TATAGGTCAC CTGGTTGGAC CTAGGTCTCG TCGACGACCT
191  C  F  W  E  G  A  K  L  Q  G  G  S  A  Y  L  P  G  R  P  D  I  Q  W  T  N  L  D  P  E  Q  L  L  E
```

FIG. 1A

```
901 GGAGCTGGGT CCCTTTGCCT CCCTTGAGGG CTTCCGGGAG CTGCTAGACA AGGCACAGGT GGGCCAGGCC TACGTGGGGC GGCCCTGTCT GCACCCTGAT
    CCTCGACCCA GGGAAACGGA GGGAACTCCC GAAGGCCCTC GACGATCTGT TCCGTGTCCA CCCGGTCCGG ATGCACCCCG CCGGGACAGA CGTGGGACTA
224 E L G P F A S L E G F R E L L D K A Q V G Q A Y V G R P C L H P D

1001 GACCTCCACT GCCCACCTAG TGCCCCCAAC CATCACAGCA GGCAGGCTCC CAATGTGGCT CACGAGCTGA GTGGGGGCTG CCATGGCTTC TCCCACAAAT
     CTGGAGGTGA CGGGTGGATC ACGGGGGTTG GTAGTGTCGT CCGTCCGAGG GTTACACCGA GTGCTCGACT CACCCCCGAC GGTACCGAAG AGGGTGTTTA
257  D L H C P P S A P N H H S R Q A P N V A H E L S G G C H G F S H K F

1101 TCATGCACTG GCAGGAGGAA TTGCTGCTGG GAGGCATGGC CAGAGACCCC CAAGGAGAGC TGCTGAGGGC AGAGGCCCTG CAGAGCACCT TCTTGCTGAT
     AGTACGTGAC CGTCCTCCTT AACGACGACC CTCCGTACCG GTCTCTGGGG GTTCCTCTCG ACGACTCCCG TCTCCGGGAC GTCTCGTGGA AGAACGACTA
291   M H W Q E E L L L G G M A R D P Q G E L L R A E A L Q S T F L L M

1201 GAGTCCCCGC CAGCTGTACG AGCATTTCCG GGGTGACTAT CAGACACATG ACATTGGCTG GAGTGAGGAG CAGGCCAGCA CAGTGCTACA AGCCTGGCAG
     CTCAGGGGCG GTCGACATGC TCGTAAAGGC CCCACTGATA GTCTGTGTAC TGTAACCGAC CTCACTCCTC GTCCGGTCGT GTCACGATGT TCGGACCGTC
324  S P R Q L Y E H F R G D Y Q T H D I G W S E E Q A S T V L Q A W Q

1301 CGGCGCTTTG TGCAGCTGGC CCAGGAGGCC CTGCCTGAGA ACGCTTCCCA GCAGATCCAT GCCTTCTCCT CCACCACCCT GGATGACATC CTGCATGCGT
     GCCGCGAAAC ACGTCGACCG GGTCCTCCGG GACGGACTCT TGCGAAGGGT CGTCTAGGTA CGGAAGAGGA GGTGGTGGGA CCTACTGTAG GACGTACGCA
357  R R F V Q L A Q E A L P E N A S Q Q I H A F S S T T L D D I L H A F

1401 TCTCTGAAGT CAGTGCTGCC CGTGTGGTGG GAGGCTATCT GCTCATGCTG GCCTATGCCT GTGTGACCAT GCTGCGGTGG GACTGCGCCC AGTCCCAGGG
     AGAGACTTCA GTCACGACGG GCACACCACC CTCCGATAGA CGAGTACGAC CGGATACGGA CACACTGGTA CGACGCCACC CTGACGCGGG TCAGGGTCCC
391   S E V S A A R V V G G Y L L M L A Y A C V T M L R W D C A Q S Q G

1501 TTCCGTGGGC CTTGCCGGGG TACTGCTGGT GGCCCTGGCG GTGGCCTCAG GCCTTGGGCT CTGTGCCCTG CTCGGCATCA CCTTCAATGC TGCCACTACC
     AAGGCACCCG GAACGGCCCC ATGACGACCA CCGGGACCGC CACCGGAGTC CGGAACCCGA GACACGGGAC GAGCCGTAGT GGAAGTTACG ACGGTGATGG
424  S V G L A G V L L V A L A V A S G L G L C A L L G I T F N A A T T

1601 CAGGTGCTGC CTTTCTTGGC TCTGGGAATC GGCGTGGATG ACGTATTCCT GCTGGCGCAT GCCTTCACAG AGGCTCTGCC TGGCACCCCT CTCCAGGAGC
     GTCCACGACG GAAAGAACCG AGACCCTTAG CCGCACCTAC TGCATAAGGA CGACCGCGTA CGGAAGTGTC TCCGAGACGG ACCGTGGGGA GAGGTCCTCG
457  Q V L P F L A L G I G V D D V F L L A H A F T E A L P G T P L Q E R

1701 GCATGGGCGA GTGTCTGCAG CGCACGGGCA CCAGTGTCGT ACTCACATCC ATCAACAACA TGGCCGCCTT CCTCATGGCT GCCCTCGTTC CCATCCCTGC
     CGTACCCGCT CACAGACGTC GCGTGCCCGT GGTCACAGCA TGAGTGTAGG TAGTTGTTGT ACCGGCGGAA GGAGTACCGA CGGGAGCAAG GGTAGGGACG
491   M G E C L Q R T G T S V V L T S I N N M A A F L M A A L V P I P A
```

FIG. 1B

```
1801 GCTGCGAGCC TTCTCCCTAC AGGCGGCCAT AGTGGTTGGC TGCACCTTTG TAGCCGTGAT GCTTGTCTTC CCAGCCATCC TCAGCCTGGA CCTACGGCGG
     CGACGCTCGG AAGAGGGATG TCCGCCGGTA TCACCAACCG ACGTGGAAAC ATCGGCACTA CGAACAGAAG GGTCGGTAGG AGTCGGACCT GGATGCCGCC
 524 L  R  A  F  S  L  Q  A  A  I  V  V  G  C  T  F  V  A  V  M  L  V  F  P  A  I  L  S  L  D  L  R  R

1901 CGCCACTGCC AGCGCCTTGA TGTGCTCTGC TGCTTCTCCA GTCCCTGCTC TGCTCAGGTG ATTCAGATCC TGCCCCAGGA GCTGGGGGAC GGGACAGTAC
     GCGGTGACGG TCGCGGAACT ACACGAGACG ACGAAGAGGT CAGGGACGAG ACGAGTCCAC TAAGTCTAGG ACGGGGTCCT CGACCCCCTG CCCTGTCATG
 557 R  H  C  Q  R  L  D  V  L  C  C  F  S  S  P  C  S  A  Q  V  I  Q  I  L  P  Q  E  L  G  D  G  T  V  P

2001 CAGTGGGCAT TGCCCACCTC ACTGCCACAG TTCAAGCCTT TACCCACTGT GAAGCCAGCA GCCAGCATGT GGTCACCATC CTGCCTCCCC AAGCCCACCT
     GTCACCCGTA ACGGGTGGAG TGACGGTGTC AAGTTCGGAA ATGGGTGACA CTTCGGTCGT CGGTCGTACA CCAGTGGTAG GACGGAGGGG TTCGGGTGGA
  591 V  G  I  A  H  L  T  A  T  V  Q  A  F  T  H  C  E  A  S  S  Q  H  V  V  T  I  L  P  P  Q  A  H  L

2101 GGTGCCCCCA CCTTCTGACC CACTGGGCTC TGAGCTCTTC AGCCCTGGAG GGTCCACACG GGACCTTCTA GGCCAGGAGG AGGAGACAAG GCAGAAGGCA
     CCACGGGGGT GGAAGACTGG GTGACCCGAG ACTCGAGAAG TCGGGACCTC CCAGGTGTGC CCTGGAAGAT CCGGTCCTCC TCCTCTGTTC CGTCTTCCGT
  624 V  P  P  P  S  D  P  L  G  S  E  L  F  S  P  G  G  S  T  R  D  L  L  G  Q  E  E  E  T  R  Q  K  A

2201 GCCTGCAAGT CCCTGCCCTG TGCCCGCTGG AATCTTGCCC ATTTCGCCCG CTATCAGTTT GCCCCGTTGC TGCTCCAGTC ACATGCCAAG GCCATCGTGC
     CGGACGTTCA GGGACGGGAC ACGGGCGACC TTAGAACGGG TAAAGCGGGC GATAGTCAAA CGGGGCAACG ACGAGGTCAG TGTACGGTTC CGGTAGCACG
  657 A  C  K  S  L  P  C  A  R  W  N  L  A  H  F  A  R  Y  Q  F  A  P  L  L  L  Q  S  H  A  K  A  I  V  L

2301 TGGTGCTCTT TGGTGCTCTT CTGGGCCTGA GCCTCTACGG AGCCACCTTG GTGCAAGACG GCCTGGCCCT GACGGATGTG GTGCCTCGGG GCACCAAGGA
     ACCACGAGAA ACCACGAGAA GACCCGGACT CGGAGATGCC TCGGTGGAAC CACGTTCTGC CGGACCGGGA CTGCCTACAC CACGGAGCCC CGTGGTTCCT
  691 V  L  F  G  A  L  L  G  L  S  L  Y  G  A  T  L  V  Q  D  G  L  A  L  T  D  V  V  P  R  G  T  K  E

2401 GCATGCCTTC CTGAGCGCCC AGCTCAGGTA CTTCTCCCTG TACGAGGTGG CCCTGGTGAC CCAGGGTGGC TTTGACTACG CCCATTCCCA ACGCGCCCTC
     CGTACGGAAG GACTCGCGGG TCGAGTCCAT GAAGAGGGAC ATGCTCCACC GGGACCACTG GGTCCCACCG AAACTGATGC GGGTAAGGGT TGCGCGGGAG
  724 H  A  F  L  S  A  Q  L  R  Y  F  S  L  Y  E  V  A  L  V  T  Q  G  G  F  D  Y  A  H  S  Q  R  A  L

2501 TTTGATCTGC ACCAGCGCTT CAGTTCCCTC AAGGCGGTGC TGCCCCCACC GGCCACCCAG GCACCCCGCA CCTGGCTGCA CTATTACCGC AACTGGCTAC
     AAACTAGACG TGGTCGCGAA GTCAAGGGAG TTCCGCCACG ACGGGGGTGG CCGGTGGGTC CGTGGGGCGT GGACCGACGT GATAATGGCG TTGACCGATG
  757 F  D  L  H  Q  R  F  S  S  L  K  A  V  L  P  P  P  A  T  Q  A  P  R  T  W  L  H  Y  Y  R  N  W  L  Q

2601 AGGGAATCCA GGCTGCCTTT GACCAGGACT GGGCTTCTGG GCGCATCACC CGCCACTCGT ACCGCAATGG CTCTGAGGAT GGGGCCCTGG CCTACAAGCT
     TCCCTTAGGT CCGACGGAAA CTGGTCCTGA CCCGAAGACC CGCGTAGTGG GCGGTGAGCA TGGCGTTACC GAGACTCCTA CCCCGGGACC GGATGTTCGA
  791 G  I  Q  A  A  F  D  Q  D  W  A  S  G  R  I  T  R  H  S  Y  R  N  G  S  E  D  G  A  L  A  Y  K  L
```

FIG. 1C

```
2701 GCTCATCCAG ACTGGAGACG CCCAGGAGCC TCTGGATTTC AGCCAGCTGA CCACAAGGAA GCTGGTGGAC AGAGAGGGAC TGATTCCACC CGAGCTCTTC
     CGAGTAGGTC TGACCTCTGC GGGTCCTCGG AGACCTAAAG TCGGTCGACT GGTGTTCCTT CGACCACCTG TCTCTCCCTG ACTAAGGTGG GCTCGAGAAG
 824 L  I  Q  T  G  D  A  Q  E  P  L  D  F  S  Q  L  T  T  R  K  L  V  D  R  E  G  L  I  P  P  E  L  F

2801 TACATGGGGC TGACCGTGTG GGTGAGCAGT GACCCCCTGG GTCTGGCAGC CTCACAGGCC AACTTCTACC CCCCACCTCC TGAATGGCTG CACGACAAAT
     ATGTACCCCG ACTGGCACAC CCACTCGTCA CTGGGGGACC CAGACCGTCG GAGTGTCCGG TTGAAGATGG GGGGTGGAGG ACTTACCGAC GTGCTGTTTA
 857 Y  M  G  L  T  V  W  V  S  S  D  P  L  G  L  A  A  S  Q  A  N  F  Y  P  P  P  P  E  W  L  H  D  K  Y

2901 ACGACACCAC GGGGGAGAAC CTTCGCATCC CGCCAGCTCA GCCCTTGGAG TTTGCCCAGT TCCCCTTCCT GCTGCGTGGC CTCCAGAAGA CTGCAGACTT
     TGCTGTGGTG CCCCCTCTTG GAAGCGTAGG GCGGTCGAGT CGGGAACCTC AAACGGGTCA AGGGGAAGGA CGACGCACCG GAGGTCTTCT GACGTCTGAA
  891 D  T  T  G  E  N  L  R  I  P  P  A  Q  P  L  E  F  A  Q  F  P  F  L  L  R  G  L  Q  K  T  A  D  F

3001 TGTGGAGGCC ATCGAGGGGG CCCGGGCAGC ATGCGCAGAG GCCGGCCAGG CTGGGGTGCA CGCCTACCCC AGCGGCTCCC CCTTCCTCTT CTGGGAACAG
     ACACCTCCGG TAGCTCCCCC GGGCCCGTCG TACGCGTCTC CGGCCGGTCC GACCCCACGT GCGGATGGGG TCGCCGAGGG GGAAGGAGAA GACCCTTGTC
  924 V  E  A  I  E  G  A  R  A  A  C  A  E  A  G  Q  A  G  V  H  A  Y  P  S  G  S  P  F  L  F  W  E  Q

3101 TATCTGGGCC TGCGGCGCTG CTTCCTGCTG GCCGTCTGCA TCCTGCTGGT GTGCACTTTC CTCGTCTGTG CTCTGCTGCT CCTCAACCCC TGGACGGCTG
     ATAGACCCGG ACGCCGCGAC GAAGGACGAC CGGCAGACGT AGGACGACCA CACGTGAAAG GAGCAGACAC GAGACGACGA GGAGTTGGGG ACCTGCCGAC
  957 Y  L  G  L  R  R  C  F  L  L  A  V  C  I  L  L  V  C  T  F  L  V  C  A  L  L  L  L  N  P  W  T  A  G

3201 GCCTCATAGT GCTGGTCCTG GCGATGATGA CAGTGGAACT CTTTGGTATC ATGGGTTTCC TGGGCATCAA GCTGAGTGCC ATCCCCGTGG TGATCCTTGT
     CGGAGTATCA CGACCAGGAC CGCTACTACT GTCACCTTGA GAAACCATAG TACCCAAAGG ACCCGTAGTT CGACTCACGG TAGGGGCACC ACTAGGAACA
  991 L  I  V  L  V  L  A  M  M  T  V  E  L  F  G  I  M  G  F  L  G  I  K  L  S  A  I  P  V  V  I  L  V

3301 GGCCTCTGTA GGCATTGGCG TTGAGTTCAC AGTCCACGTG GCTCTGGGCT TCCTGACCAC CCAGGGCAGC CGGAACCTGC GGGCCGCCCA TGCCCTTGAG
     CCGGAGACAT CCGTAACCGC AACTCAAGTG TCAGGTGCAC CGAGACCCGA AGGACTGGTG GGTCCCGTCG GCCTTGGACG CCCGGCGGGT ACGGGAACTC
 1024 A  S  V  G  I  G  V  E  F  T  V  H  V  A  L  G  F  L  T  T  Q  G  S  R  N  L  R  A  A  H  A  L  E

3401 CACACATTTG CCCCCGTGAC CGATGGGGCC ATCTCCACAT TGCTGGGTCT GCTCATGCTT GCTGGTTCCC ACTTTGACTT CATTGTAAGG TACTTCTTTG
     GTGTGTAAAC GGGGGCACTG GCTACCCCGG TAGAGGTGTA ACGACCCAGA CGAGTACGAA CGACCAAGGG TGAAACTGAA GTAACATTCC ATGAAGAAAC
 1057 H  T  F  A  P  V  T  D  G  A  I  S  T  L  L  G  L  L  M  L  A  G  S  H  F  D  F  I  V  R  Y  F  F  A

3501 CGGCGCTGAC AGTGCTCACG CTCCTGGGCC TCCTCCATGG ACTCGTGCTG CTGCCTGTGC TGCTGTCCAT CCTGGGCCCG CCGCCAGAGG TGATACAGAT
     GCCGCGACTG TCACGAGTGC GAGGACCCGG AGGAGGTACC TGAGCACGAC GACGGACACG ACGACAGGTA GGACCCGGGC GGCGGTCTCC ACTATGTCTA
 1091 A  L  T  V  L  T  L  L  G  L  L  H  G  L  V  L  L  P  V  L  L  S  I  L  G  P  P  P  E  V  I  Q  M
```

FIG. 1D

```
3601 GTACAAGGAA AGCCCAGAGA TCCTGAGTCC ACCAGCTCCA CAGGGAGGCG GGCTTAGGTG GGGGGCATCC TCCTCCCTGC CCCAGAGCTT TGCCAGAGTG
     CATGTTCCTT TCGGGTCTCT AGGACTCAGG TGGTCGAGGT GTCCCTCCGC CCGAATCCAC CCCCCGTAGG AGGAGGGACG GGGTCTCGAA ACGGTCTCAC
1124  Y  K  E  S  P  E  I  L  S  P  P  A  P  Q  G  G  G  L  R  W  G  A  S  S  S  L  P  Q  S  F  A  R  V

3701 ACTACCTCCA TGACCGTGGC CATCCACCCA CCCCCCCTGC CTGGTGCCTA CATCCATCCA GCCCCTGATG AGCCCCCTTG GTCCCCTGCT GCCACTAGCT
     TGATGGAGGT ACTGGCACCG GTAGGTGGGT GGGGGGGACG GACCACGGAT GTAGGTAGGT CGGGGACTAC TCGGGGGAAC CAGGGGACGA CGGTGATCGA
1157  T  T  S  M  T  V  A  I  H  P  P  P  L  P  G  A  Y  I  H  P  A  P  D  E  P  P  W  S  P  A  A  T  S  S

3801 CTGGCAACCT CAGTTCCAGG GGACCAGGTC CAGCCACTGG GTGAAAGAGC AGCTGAAGCA CAGAGACCAT GTGTGGGGCG TGTGGGGTCA CTGGGAAGCA
     GACCGTTGGA GTCAAGGTCC CCTGGTCCAG GTCGGTGACC CACTTTCTCG TCGACTTCGT GTCTCTGGTA CACACCCCGC ACACCCCAGT GACCCTTCGT
1191   G  N  L  S  S  R  G  P  G  P  A  T  G  O
                                        \ 1203

3901 CTGGGTCTGG TGTTAGACGC AGGACGGACC CCTGGAGGGC CCTGCTGCTG CTGCATCCCC TCTCCCGACC CAGCTGTCAT GGGCCTCCCT GATATCGAAT
     GACCCAGACC ACAATCTGCG TCCTGCCTGG GGACCTCCCG GGACGACGAC GACGTAGGGG AGAGGGCTGG GTCGACAGTA CCCGGAGGGA CTATAGCTTA
                          ^T to C  (silent)                    pRK follows, this is the 5prime end of vector^

4001 TCAATCGATA GAACCGAGGT GCAGTTGGAC
     AGTTAGCTAT CTTGGCTCCA CGTCAACCTG
```

FIG. 1E

(SEQ ID NO: 3)

(SEQ ID NO: 4)

```
                    30        40        50        60        70
905531        GCTGGGGTGCACGCCTACCNCAGCGGNTCCCCCTTCCTCTTCTGGAACA
                 ::: ::  :   ******* ***** ****************** **
hpatched      CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGGAGCA
           3010      3020      3030      3040      3050

                    80        90       100       110       120
905531        GTATCTGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGG
              ***  * ***** ** * ***  * ******  * ** ** *  ** ***
hpatched      GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTCATCAGCGTGGTGTTGG
           3060      3070      3080      3090      3100

                   130       140       150       160       170
905531        TGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTNAACCCCTGGACGGCT
                ***** ******** ** *** *  * ** *****************
hpatched      CCTGCACATTCCTCGTGTGCGCTGTCTTCCTTCTGAACCCCTGGACGGCC
           3110      3120      3130      3140      3150

                   180       190       200       210       220
905531        GGCCTNATAGTGCTGGTCCTGGCGATGATGACAGTGGAACTCTTTGGTAT
              **  **** *** *********** ******* ** ** ** ** ** **
hpatched      GGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTGTTCGGCAT
           3160      3170      3180      3190      3200

                   230       240       250
905531        CATGGGTTTNCTGGGCATCAAGCTGAGT
               *****  ** * ** ******** ***
hpatched      GATGGGCCTCATCGGAATCAAGCTCAGT
           3210      3220      3230


                 80        90       100       110       120
905531        TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGT
               :::   :::     * ** *  ** *****   ****   * ** ****
hpatched      GCTGCTGCTGTTCATCAGCGTGGTGTTGGCC---TGCACATTCCTCGTGT
                    3090      3100      3110         3120

                130       140       150
905531        GCACTTTCCTCGTCTGTGCTCTGCTGCT
              ** ** ** ** *       :    :
hpatched      GCGCTGTCTTCCTTCTGAACCCCTGGAC
             3130      3140      3150
```

FIG. 2A

```
                                   30        40        50        60        70
(SEQ ID NO: 5) 1326258    GCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACA
                              ::: ::  :     ******* ***** ***************** **
               hpatched   CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCA
                             3010      3020      3030      3040      3050

                                   80        90       100       110       120
               1326258    GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGG
                          ***  * ***** ** * ***  * ******  * ** ** *   ** ***
               hpatched   GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTCATCAGCGTGGTGTTGG
                             3060      3070      3080      3090      3100

                                  130       140       150
               1326258    TGTGCACTTTCCTCNTCTGTGCTCT
                            ***** ******** ** *** *
               hpatched   CCTGCACATTCCTCGTGTGCGCTGT
                             3110      3120      3130


                                         90       100       110       120       130
               1326258    TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGT
                           :::    :::      * ** *  ** *****    ****   * ** ****
               hpatched   GCTGCTGCTGTTCATCAGCGTGGTGTTGGCC---TGCACATTCCTCGTGT
                                3090      3100      3110          3120

                                       140       150
               1326258    GCACTTTCCTCNTCTGTGCTCT
                          ** ** ** ****        :
               hpatched   GCGCTGTCTTCCTTCTGAACCC
                             3130      3140


                                     10        20        30        40        50
               1326258    CCGGGCAGCATGCGCAGAGGCCGGCCAGGCTGGGGTGCACGCCTACCCCA
                          ****** *****      ** ** * *** ******* *        :
(SEQ ID NO 6)  hpatched.RC  CCGGGCGGCATG--GCGAAGCGGACCACGCTGGGGGTGGCTCAGGGGAG
                            710       720           730       740       750
```

FIG. 2B

(SEQ ID NO:4)
(SEQ ID NO:2)

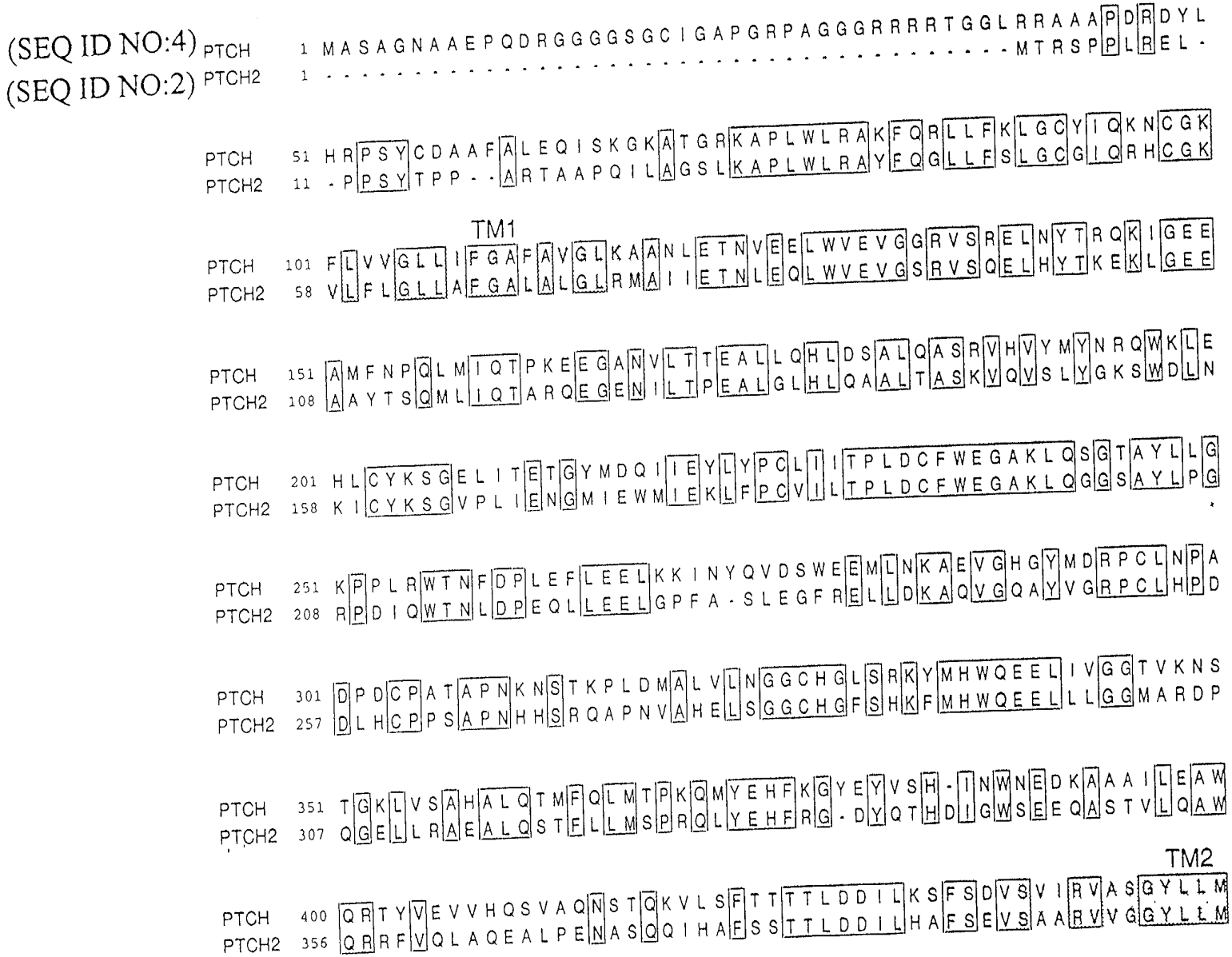

FIG. 3A


TM3
TM4
TM5
TM6
TM7
PTCH 450 LAYACLTMLRWDCSKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAAT
PTCH2 406 LAYACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGITFNAAT
PTCH 500 TQVLPFLALGVGVDDVFLLAHAFSETGQNKRIPFEDRTGECLKRTGASVA
PTCH2 456 TQVLPFLALGIGVDDVFLLAHAFTEALPG--TPLQERMGECLQRTGTSVV
PTCH 550 LTSISNVTAFFMAALIPIPALRAFSLQAAVVVFNFAMVLLIFPAILSMD
PTCH2 504 LTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAILSLD
PTCH 600 LYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHS
PTCH2 554 LRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGT----------VPVG
PTCH 650 FAHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSC
PTCH2 593 IAH----LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGS
PTCH 700 QSPESTSSTRDLLSQFSDSSLH--CLEPPCTKWTLSSFAEKHYAPFLLKP
PTCH2 634 ELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQS
PTCH 748 KAKVVVIFLFLGLLGVSLYGTTRVRDGLDLTDIVPRETREYDFIAAQFKY
PTCH2 684 HAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRY
PTCH 798 FSFYNMYIVTQKA-DYPNIQHLLYDLHRSFSNVKYVMLEENKQLPKMWLH
PTCH2 734 FSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRTWLH

FIG. 3B

```
                                                 ***
PTCH    847  YFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLLVQTGSRDKP
PTCH2   784  YYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEP

PTCH    897  IDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRP
PTCH2   834  LDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPP

PTCH    947  EWVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRT
PTCH2   884  EWLHDKYD-TTGENLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARA
                                                        TM8
PTCH    997  ICSNYTSLGLSSYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVF
PTCH2   933  ACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALL
                        TM9                                TM10
PTCH   1047  LLNPWTAGIIVMVLALMTVELFGMMGLIGIKLSAVPVVILIASVGIGVEF
PTCH2   983  LLNPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASVGIGVEF
                                                  TM11
PTCH   1097  TVHVALAFLTAIGDKNRRAVLALEHMFAPVLDGAVSTLLGVLMLAGSEFD
PTCH2  1033  TVHVALGFLTTQGSRNLRAAHALEHTFAPVTDGAISTLLGLLMLAGSHFD
                            TM12
PTCH   1147  FIVRYFFAVLAILTILGVLNGLVLLPVLLSFFGPYPEVSPANGLNRLPTP
PTCH2  1083  FIVRYFFAALTVLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILS

PTCH   1197  SPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSEELRHYEAQQG
PTCH2  1133  PPAPQGGGLRWGASSSLPQS-FARVTTSMTVAIHPPPLPGAYIHPAPDEP
```

FIG. 3C

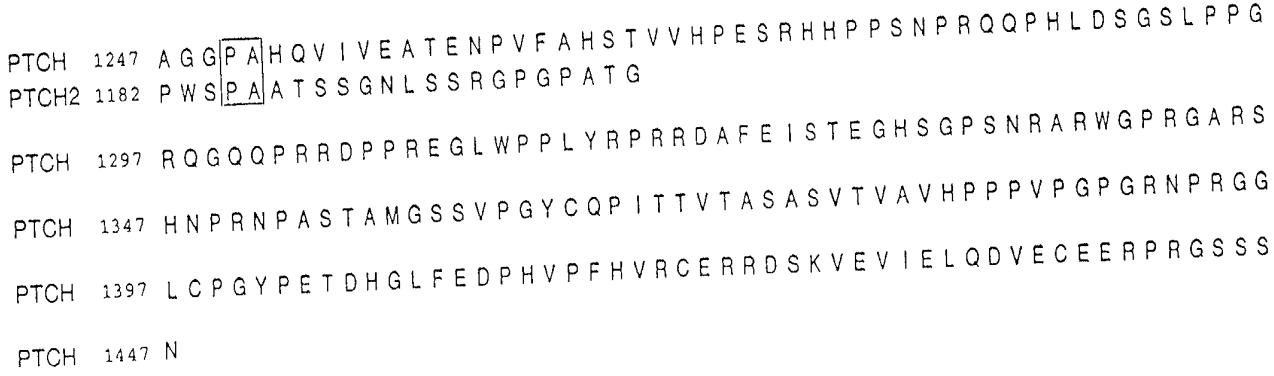
PTCH 1247 AGGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPG
PTCH2 1182 PWSPAATSSGNLSSRGPGPATG
PTCH 1297 RQGQQPRRDPPREGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARS
PTCH 1347 HNPRNPASTAMGSSVPGYCQPITTVTASASVTVAVHPPPVPGPGRNPRGG
PTCH 1397 LCPGYPETDHGLFEDPHVPFHVRCERRDSKVEVIELQDVECEERPRGSSS
PTCH 1447 N

FIG. 3D

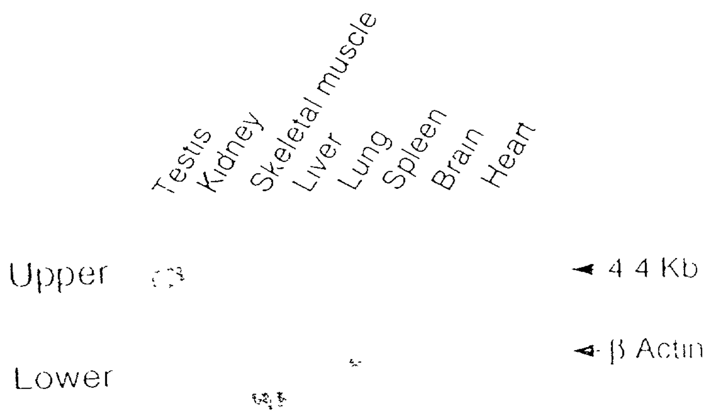
Testis
Kidney
Skeletal muscle
Liver
Lung
Spleen
Brain
Heart
Upper
Lower
4.4 Kb
β Actin

FIG. 4

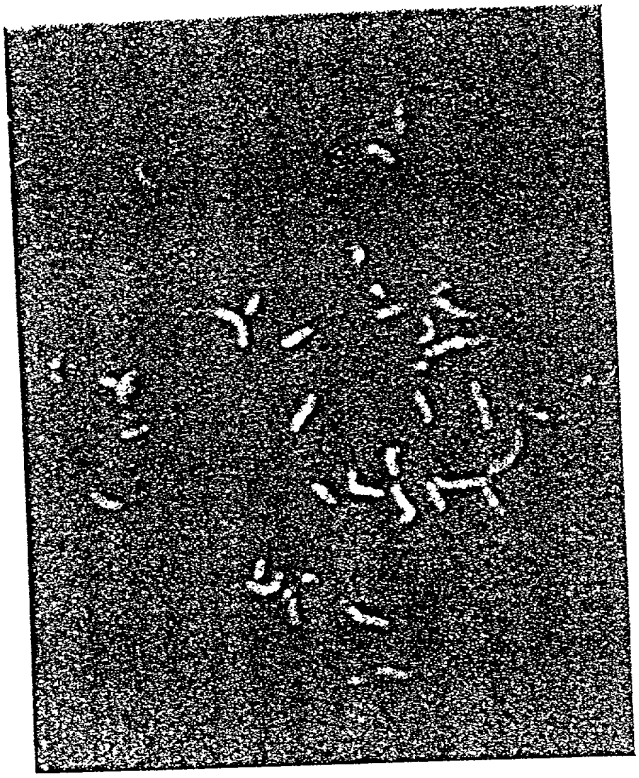

FIG. 5

FIG. 6A

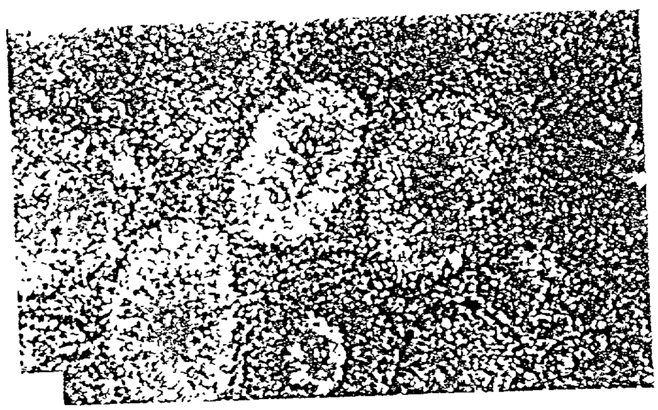

FIG. 6B

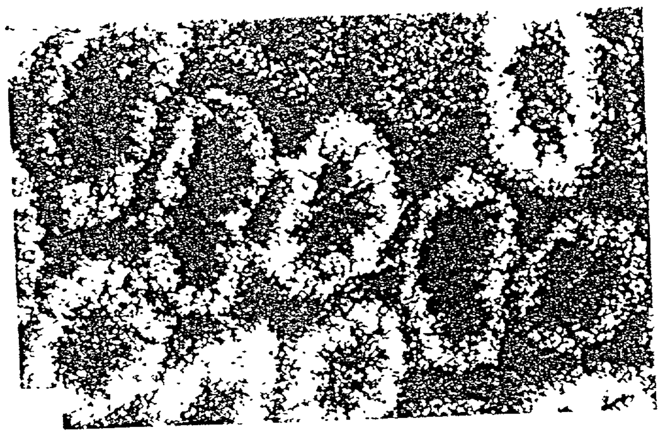

FIG. 6C

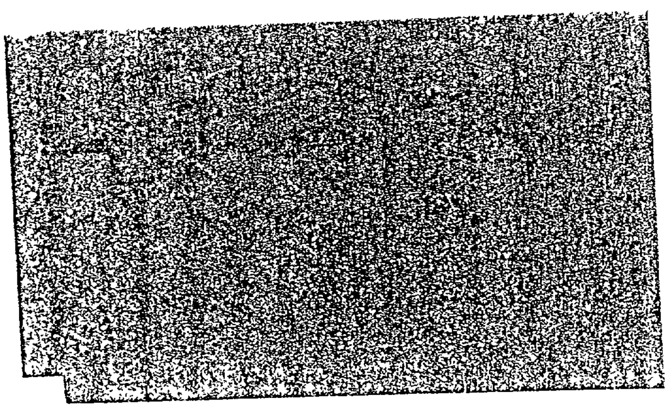

FIG. 6D

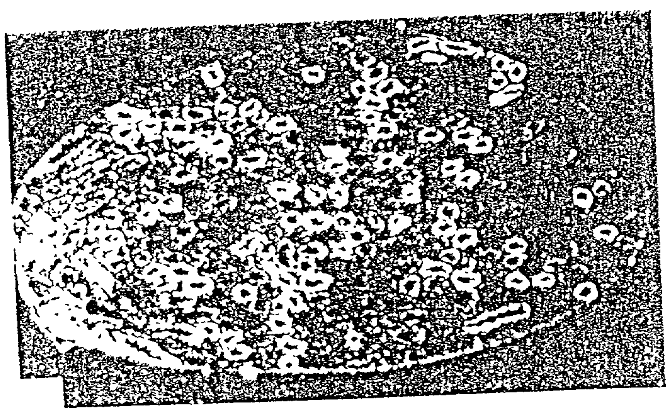

FIG. 6E

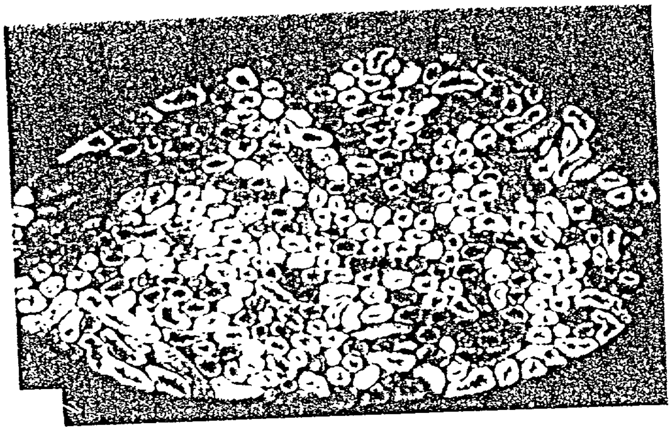

FIG. 6F

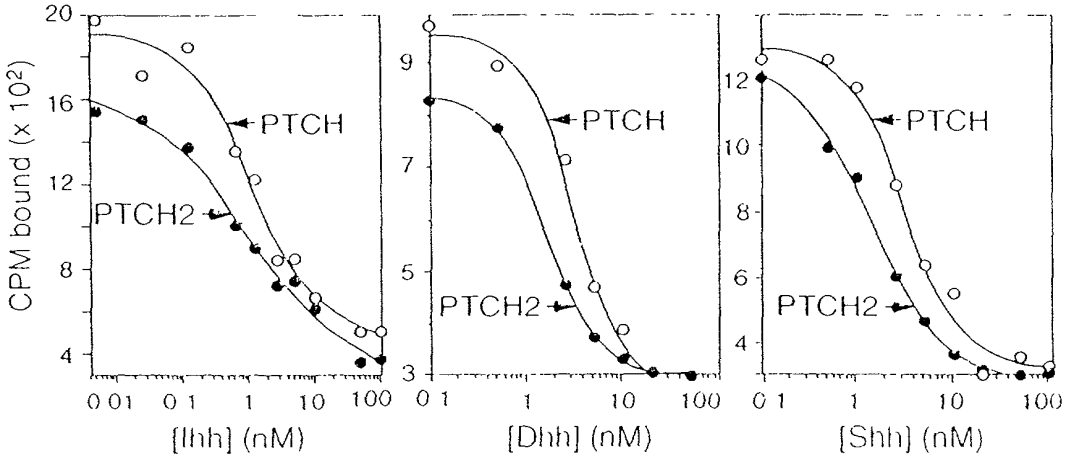

FIG. 7A

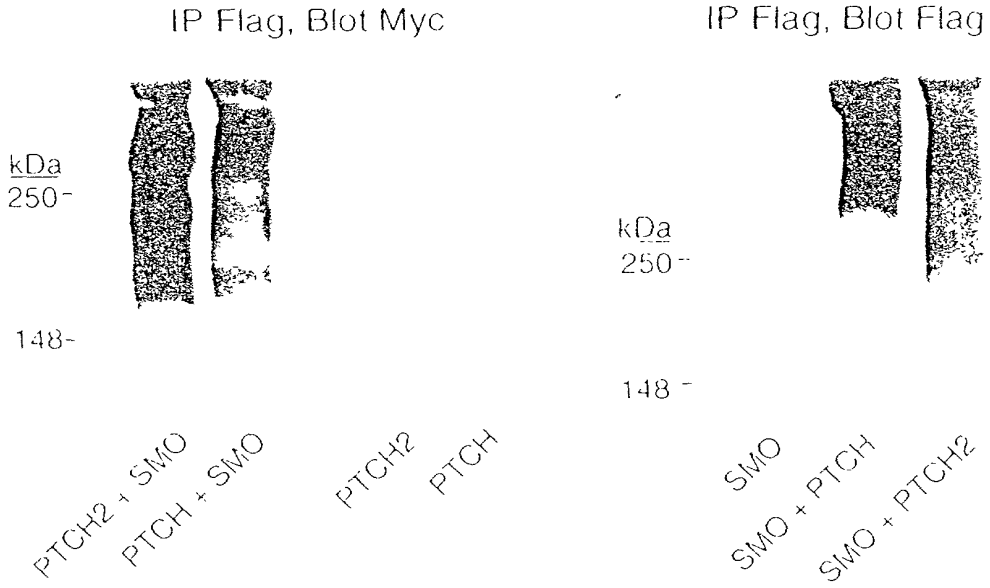

FIG. 7B

```
                     10        20        30        40        50
hPtch-2      MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCG
             * *. .* ***********..**.******.****************** 
mPatched2    MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCR
(SEQ ID NO:7)        10        20        30        40        50

                     60        70        80        90       100
hPtch-2      IQRHCGKVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYT
             **.**********.**********.*.***.*******************
mPatched2    IQKHCGKVLFLGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYT
                     60        70        80        90       100

                    110       120       130       140       150
hPtch-2      KEKLGEEAAYTSQMLIQTARQEGENILTPEALGLHLQAALTASKVQVSLY
             *******************.*** *.******.*****************
mPatched2    KEKLGEEAAYTSQMLIQTAHQEGGNVLTPEALDLHLQAALTASKVQVSLY
                    110       120       130       140       150

                    160       170       180       190       200
hPtch-2      GKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTPLDCFWEGAKLQG
             ************************.*************************
mPatched2    GKSWDLNKICYKSGVPLIENGMIERMIEKLFPCVILTPLDCFWEGAKLQG
                    160       170       180       190       200

                    210       220       230       240       250
hPtch-2      GSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDKAQVGQAYVGR
             ******************.*******************************
mPatched2    GSAYLPGRPDIQWTNLDPQQLLEELGPFASLEGFRELLDKAQVGQAYVGR
                    210       220       230       240       250

                    260       270       280       290       300
hPtch-2      PCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG
             ***.*** ********.*********.***********************
mPatched2    PCLDPDDPHCPPSAPNRHSRQAPNVAQELSGGCHGFSHKFMHWQEELLLG
                    260       270       280       290       300

                    310       320       330       340       350
hPtch-2      GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQAST
             * *** **.****************************************
mPatched2    GTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASM
                    310       320       330       340       350
```

FIG. 8A

```
                   360       370       380       390       400
hPtch-2     VLQAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVG
            ****************** ******************.******..****
mPatched2   VLQAWQRRFVQLAQEALPANASQQIHAFSSTTLDDILRAFSEVSTTRVVG
                   360       370       380       390       400

                   410       420       430       440       450
hPtch-2     GYLLMLAYACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGIT
            ***********************.**************************
mPatched2   GYLLMLAYACVTMLRWDCAQSQGAVGLAGVLLVALAVASGLGLCALLGIT
                   410       420       430       440       450

                   460       470       480       490       500
hPtch-2     FNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGT
            ********************.******** * *.*** *******. ***
mPatched2   FNAATTQVLPFLALGIGVDDIFLLAHAFTKAPPDTPLPERMGECLRSTGT
                   460       470       480       490       500

                   510       520       530       540       550
hPtch-2     SVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAIL
            ** ***.*** **.*********************** * **********
mPatched2   SVALTSVNNMVAFFMAALVPIPALRAFSLQAAIVVGCNFAAVMLVFPAIL
                   510       520       530       540       550

                   560       570       580       590       600
hPtch-2     SLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV
            ******** *******************.******* .************
mPatched2   SLDLRRRHRQRLDVLCCFSSPCSAQVIQMLPQELGDRAVPVGIAHLTATV
                   560       570       580       590       600

                   610       620       630       640       650
hPtch-2     QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEE
            ***********************..*.********.**********.***
mPatched2   QAFTHCEASSQHVVTILPPQAHLLSPASDPLGSELYSPGGSTRDLLSQEE
                   610       620       630       640       650

                   660       670       680       690       700
hPtch-2     ETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLS
             *  .***..* **.* ***************..***.**..********
mPatched2   GTGPQAACRPLLCAHWTLAHFARYQFAPLLLQTRAKALVLLFFGALLGLS
                   660       670       680       690       700
```

FIG. 8B

```
                  710       720       730       740       750
hPtch-2    LYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYA
           **************************************************
mPatched2  LYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYA
                  710       720       730       740       750

                  760       770       780       790       800
hPtch-2    HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDW
           ************************************.*************
mPatched2  HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRSWLQGIQAAFDQDW
                  760       770       780       790       800

                  810       820       830       840       850
hPtch-2    ASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGL
           ****** *********************.******************.***
mPatched2  ASGRITCHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLTTRKLVDKEGL
                  810       820       830       840       850

                  860       870       880       890       900
hPtch-2    IPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP
           **************************************************
mPatched2  IPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP
                  860       870       880       890       900

                  910       920       930       940       950
hPtch-2    PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSP
           .*************.*******************.***************
mPatched2  AAQPLEFAQFPFLLHGLQKTADFVEAIEGARAACTEAGQAGVHAYPSGSP
                  910       920       930       940       950

                  960       970       980       990      1000
hPtch-2    FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMT
           **********************************.***************
mPatched2  FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLSPWTAGLIVLVLAMMT
                  960       970       980       990      1000

                 1010      1020      1030      1040      1050
hPtch-2    VELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLR
           *************************.****************..******
mPatched2  VELFGIMGFLGIKLSAIPVVILVASIGIGVEFTVHVALGFLTSHGSRNLR
                 1010      1020      1030      1040      1050
```

FIG. 8C

```
                   1060      1070      1080      1090      1100
hPtch-2     AAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGL
            ** ***.*********.************.****.****  *********
mPatched2   AASALEQTFAPVTDGAVSTLLGLLMLAGSNFDFIIRYFFVVLTVLTLLGL
                   1060      1070      1080      1090      1100

                   1110      1120      1130      1140      1150
hPtch-2     LHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGGLRWGASSSLP
            ****.*************.*.*.*****. *...*** *****. ...**
mPatched2   LHGLLLLPVLLSILGPPPQVVQVYKESPQTLNSAAPQRGGLRWDRPPTLP
                   1110      1120      1130      1140      1150

                   1160      1170      1180      1190      1200
hPtch-2     QSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP
            *************.*********.***..**
mPatched2   QSFARVTTSMTVALHPPPLPGAYVHPASEEPT
                   1160      1170      1180

hPtch-2     ATG
```

FIG. 8D

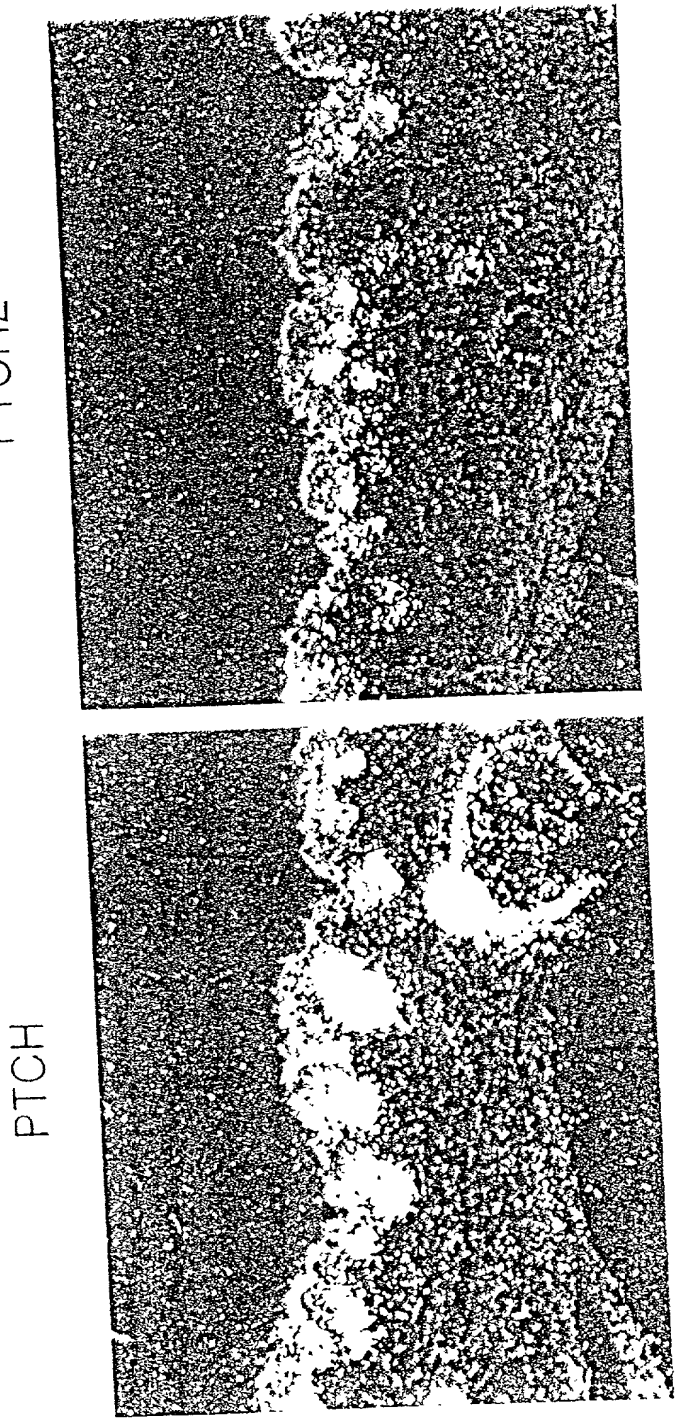

FIG. 9

> Consensus Sequence of human patched 2 cDNA clone
> length: 4004 bp

(SEQ ID NO:8)

```
   1 CCCACGCGTC CGGGAGAAGC TGGGGGAGGA GGCTGCATAC ACCTCTCAGA TGCTGATACA GACCGCACGC CAGGAGGGAG AGAACATCCT CACACCCGAA
     GGGTGCGCAG GCCCTCTTCG ACCCCCTCCT CCGACGTATG TGGAGAGTCT ACGACTATGT CTGGCGTGCG GTCCTCCCTC TCTTGTAGGA GTGTGGGCTT
                                                  race 6

 101 GCACTTGGCC TCCACCTCCA GGCAGCCCTC ACTGCCAGTA AAGTCCAAGT ATCACTCTAT GGGAAGTCCT GGGATTTGAA CAAAATCTGC TACAAGTCAG
     CGTGAACCGG AGGTGGAGGT CCGTCGGGAG TGACGGTCAT TTCAGGTTCA TAGTGAGATA CCCTTCAGGA CCCTAAACTT GTTTTAGACG ATGTTCAGTC
                                                                                                  race 5'

 201 GAGTTCCCCT TATTGAAAAT GGAATGATTG AGCGGATGAT TGAGAAGCTG TTTCCGTGCG TGATCCTCAC CCCCCTCGAC TGCTTCTGGG AGGGAGCCAA
     CTCAAGGGGA ATAACTTTTA CCTTACTAAC TCGCCTACTA ACTCTTCGAC AAAGGCACGC ACTAGGAGTG GGGGGAGCTG ACGAAGACCC TCCCTCGGTT

 301 ACTCCAAGGG GGCTCCGCCT ACCTGCCGCT CCCAATGTGG CTCACGAGCT GAGTGGGGGC TGCCATGGCT TCTCCCACAA ATTCATGCAC TGGCAGGAGG
     TGAGGTTCCC CCGAGGCGGA TGGACGGCGA GGGTTACACC GAGTGCTCGA CTCACCCCCG ACGGTACCGA AGAGGGTGTT TAAGTACGTG ACCGTCCTCC

 401 AATTGCTGCT GGGAGGCATG GCCAGAGACC CCCAAGGAGA GCTGCTGAGG GCAGAGGCCC TGCAGAGCAC CTTCTTGCTG ATGAGTCCCC GCCAGCTGTA
     TTAACGACGA CCCTCCGTAC CGGTCTCTGG GGGTTCCTCT CGACGACTCC CGTCTCCGGG ACGTCTCGTG GAAGAACGAC TACTCAGGGG CGGTCGACAT

 501 CGAGCATTTC CGGGGTGACT ATCAGACACA TGACATTGGC TGGAGTGAGG AGCAGGCCAG CACAGTGCTA CAAGCCTGGC AGCGGCGCTT TGTGCAGGTC
     GCTCGTAAAG GCCCCACTGA TAGTCTGTGT ACTGTAACCG ACCTCACTCC TCGTCCGGTC GTGTCACGAT GTTCGGACCG TCGCCGCGAA ACACGTCCAG

 601 GGTATGGACA AGGACAGGGG GGTGCCCTGA GGCCATTCCC TCCTCCTGCC CCCTCCTATC CACCCTGTTT CTCCAGCTGG CCCAGGAGGC CCTGCCTGAG
     CCATACCTGT TCCTGTCCCC CCACGGGACT CCGGTAAGGG AGGAGGACGG GGGAGGATAG GTGGGACAAA GAGGTCGACC GGGTCCTCCG GGACGGACTC

 701 AACGCTTCCC AGCAGATCCA TGCCTTCTCC TCCACCACCC TGGATGACAT CCTGCATGCG TTCTCTGAAG TCAGTGCTGC CCGTGTGGTG GGAGGCTATC
     TTGCGAAGGG TCGTCTAGGT ACGGAAGAGG AGGTGGTGGG ACCTACTGTA GGACGTACGC AAGAGACTTC AGTCACGACG GGCACACCAC CCTCCGATAG

 801 TGCTCATGGT GGGTCTTGCA CCTGGCACCT TGCCCCCACC CCACCTCCAA CCAGTGCCCA CCCTGGGGAG CCCCTGAGAC TGCCCTTTCC CCCCACAGCT
     ACGAGTACCA CCCAGAACGT GGACCGTGGA ACGGGGGTGG GGTGGAGGTT GGTCACGGGT GGGACCCCTC GGGGACTCTG ACGGGAAAGG GGGGTGTCGA
```

FIG. 10A

```
901 GGCCTATGCC TGTGTGACCA TGCTGCGGTG GGACTGCGCC CAGTCCCAGG GTTCCGTGGG CCTTGCCGGG GTACTGCTGG TGGCCCTGGC GGTGGCCTCA
    CCGGATACGG ACACACTGGT ACGACGCCAC CCTGACGCGG GTCAGGGTCC CAAGGCACCC GGAACGGCCC CATGACGACC ACCGGGACCG CCACCGGAGT

1001 GGCCTTGGGC TCTGTGCCCT GCTCGGCATC ACCTTCAATG CTGCCACTAC CCAGGTACGC CAGGACTGCA GGGCAGACTC AGTGCCAGTC ACCAGGCTTC
     CCGGAACCCG AGACACGGGA CGAGCCGTAG TGGAAGTTAC GACGGTGATG GGTCCATGCG GTCCTGACGT CCCGTCTGAG TCACGGTCAG TGGTCCGAAG

1101 ACGGGTCCTC AGCTGCCCGC TCCTCTGCCC CTCCAGGTGC TGCCCTTCTT GACTCTGGGA ATCGGCGTGG ATGACGTATT CCTGCTGGCG CATGCCTTCA
     TGCCCAGGAG TCGACGGGCG AGGAGACGGG GAGGTCCACG ACGGGAAGAA CTGAGACCCT TAGCCGCACC TACTGCATAA GGACGACCGC GTACGGAAGT

1201 CAGAGGCTCT GCCTGGCACC CCTCTCCAGG TGGGGCCTTG TCCCCCAGGG CTCATCTGAG GCAGCTCAGC TTACTGGTTA AGAGCCTCTT GGTTCAAGTG
     GTCTCCGAGA CGGACCGTGG GGAGAGGTCC ACCCCGGAAC AGGGGGTCCC GAGTAGACTC CGTCGAGTCG AATGACCAAT TCTCGGAGAA CCAAGTTCAC

1301 ACCTTGGGCT GCTAATGAAC CTCGGTGCCT CTTGTCCCCA TGTGTAAACA GGGGAAATAA TAGTGCTGTG TCCTAAGGGT TATTGTTTGG ATCAGTGAAG
     TGGAACCCGA CGATTACTTG GAGCCACGGA GAACAGGGGT ACACATTTGT CCCCTTTATT ATCACGACAC AGGATTCCCA ATAACAAACC TAGTCACTTC

1401 TAACTCAAGT TGAATGCTTA GAACAGCCCA TCATACGTAC ATGGTACCCA ATAAATGCTA GCCACTGTGT TATGACTGCC CCACCTCTGC ACCCCAAGTT
     ATTGAGTTCA ACTTACGAAT CTTGTCGGGT AGTATGCATG TACCATGGGT TATTTACGAT CGGTGACACA ATACTGACGG GGTGGAGACG TGGGGTTCAA

1501 CCTGAGCCTC CCCTTCACTC CACTTTGACA CGGCCCCTCC CTTGTGACCT GAGGGCAGGT CCCCACTCTG TCCTGGCAGG AGCGCATGGG CGAGTGTCTG
     GGACTCGGAG GGGAAGTGAG GTGAAACTGT GCCGGGGAGG GAACACTGGA CTCCCGTCCA GGGGTGAGAC AGGACCGTCC TCGCGTACCC GCTCACAGAC

1601 CAGCGCACGG GCACCAGTGT TGTACTCACA TCCATCAACA ACATGGCCGC CTTCCTCATG GCTGCCCTCG TTCCCATCCC TGCGCTGCGA GCCTTCTCCC
     GTCGCGTGCC CGTGGTCACA ACATGAGTGT AGGTAGTTGT TGTACCGGCG GAAGGAGTAC CGACGGGAGC AAGGGTAGGG ACGCGACGCT CGGAAGAGGG

1701 TACAGCCTGG ACCTACGGCG GCGCCACTGC CAGCGCCTTG ATGTGCTCTG CTGCTTCTCC AGGTACTGCC TGCGCCCCAG CCCCTTCCTC CCGTGACCCA
     ATGTCGGACC TGGATGCCGC CGCGGTGACG GTCGCGGAAC TACACGAGAC GACGAAGAGG TCCATGACGG ACGCGGGGTC GGGGAAGGAG GGCACTGGGT

1801 CGCCAGCCTG TCCCCTCACC AGCATTTCAA GGCACAGACC TGTCATCCAC TCTCTACCTC TTCCAGTCCC TGCTCTGCTC AGGTGATTCA GATCCTGCCC
     GCGGTCGGAC AGGGGAGTGG TCGTAAAGTT CCGTGTCTGG ACAGTAGGTG AGAGATGGAG AAGGTCAGGG ACGAGACGAG TCCACTAAGT CTAGGACGGG

1901 CAGGAGCTGG GGGACGGGAC AGTACCAGTG GGCATTGCCC ACCTCACTGC CACAGTTCAA GCCTTTACCC ACTGTGAAGC CAGCAGCCAG CATGTGGTCA
     GTCCTCGACC CCCTGCCCTG TCATGGTCAC CCGTAACGGG TGGAGTGACG GTGTCAAGTT CGGAAATGGG TGACACTTCG GTCGTCGGTC GTACACCAGT

2001 CCATCCTGCC TCCCCAAGCC CACCTGGTGC CCCCACCTTC TGACCCACTG GGCTCTGAGC TCTTCAGCCC TGGAGGGTCC ACACGGGACC TTCTAGGCCA
     GGTAGGACGG AGGGGTTCGG GTGGACCACG GGGGTGGAAG ACTGGGTGAC CCGAGACTCG AGAAGTCGGG ACCTCCCAGG TGTGCCCTGG AAGATCCGGT
```

FIG. 10B

```
2101 GGAGGAGGAG ACAAGGCAGA AGGCAGCCTG CAAGTCCCTG CCCTGTGCCC GCTGGAATCT TGCCCATTTC GCCCGCTATC AGTTTGCCCC GTTGCTGCTC
     CCTCCTCCTC TGTTCCGTCT TCCGTCGGAC GTTCAGGGAC GGGACACGGG CGACCTTAGA ACGGGTAAAG CGGGCGATAG TCAAACGGGG CAACGACGAG

2201 CAGTCACATG CCAAGGCCAT CGTGCTGGTG CTCTTTGGTG CTCTTCTGGG CCTGAGCCTC TACGGAGCCA CCTTGGTGCA AGACGGCCTG GCCCTGACGG
     GTCAGTGTAC GGTTCCGGTA GCACGACCAC GAGAAACCAC GAGAAGACCC GGACTCGGAG ATGCCTCGGT GGAACCACGT TCTGCCGGAC CGGGACTGCC

2301 ATGTGGTGCC TCGGGGCACC AAGGAGCATG CCTTCCTGAG CGCCCAGCTC AGGTACTTCT CCCTGTACGA GGTGGCCCTG GTGACCCAGG GTGGCTTTGA
     TACACCACGG AGCCCCGTGG TTCCTCGTAC GGAAGGACTC GCGGGTCGAG TCCATGAAGA GGGACATGCT CCACCGGGAC CACTGGGTCC CACCGAAACT

2401 CTACGCCCAC TCCCAACGCG CCCTCTTTGA TCTGCACCAG CGCTTCAGTT CCCTCAAGGC GGTGCTGCCC CCACCGGCCA CCCAGGCACC CCGCACCTGG
     GATGCGGGTG AGGGTTGCGC GGGAGAAACT AGACGTGGTC GCGAAGTCAA GGGAGTTCCG CCACGACGGG GGTGGCCGGT GGGTCCGTGG GGCGTGGACC

2501 CTGCACTATT ACCGCAACTG GCTACAGGGA ATCCAGGCTG CCTTTGACCA GGACTGGGCT TCTGGGCGCA TCACCCGCCA CTCGTACCGC AATGGCTCTG
     GACGTGATAA TGGCGTTGAC CGATGTCCCT TAGGTCCGAC GGAAACTGGT CCTGACCCGA AGACCCGCGT AGTGGGCGGT GAGCATGGCG TTACCGAGAC

2601 AGGATGGGGC CCTGGCCTAC AAGCTGCTCA TCCAGACTGG AGACGCCCAG GAGCCTCTGG ATTTCAGCCA GGTTGGGAGA GGGCTGGAGG GGTCCACTAG
     TCCTACCCCG GGACCGGATG TTCGACGAGT AGGTCTGACC TCTGCGGGTC CTCGGAGACC TAAAGTCGGT CCAACCCTCT CCCGACCTCC CCAGGTGATC

2701 TACAGGGGCT GCAGGCCTCC TGGGCCCAGG CCTTCAGCCC TCTCTGCCTC TGCAGCTGAC CACAAGGAAG CTGGTGGACA GAGAGGGACT GATTCCACCC
     ATGTCCCCGA CGTCCGGAGG ACCCGGGTCC GGAAGTCGGG AGAGACGGAG ACGTCGACTG GTGTTCCTTC GACCACCTGT CTCTCCCTGA CTAAGGTGGG

2801 GAGCTCTTCT ACATGGGGCT GACCGTGTGG GTGAGCAGTG ACCCCCTGGG TCTGGCAGCC TCACAGGCCA ACTTCTACCC CCCACCTCCT GAATGGCTGC
     CTCGAGAAGA TGTACCCCGA CTGGCACACC CACTCGTCAC TGGGGGACCC AGACCGTCGG AGTGTCCGGT TGAAGATGGG GGGTGGAGGA CTTACCGACG

2901 ACGACAAATA CGACACCACG GGGGAGAACC TTCGCAGTGA GTCTTGGGGG GAGCTCGGCA AGAGCCTCAG CCTCGCCCAC ACAAGCCCTG AGCCTGAGGC
     TGCTGTTTAT GCTGTGGTGC CCCCTCTTGG AAGCGTCACT CAGAACCCCC CTCGAGCCGT TCTCGGAGTC GGAGCGGGTG TGTTCGGGAC TCGGACTCCG

3001 CCTGCCCACT CTGCCCCGTG CTCACCGCCC TGTCCCTCTC CCTCTTCTCC CTTCCCCTCC CCTCCACAGT CCCGCCAGCT CAGCCCTTGG AGTTTGCCCA
     GGACGGGTGA GACGGGGCAC GAGTGGCGGG ACAGGGAGAG GGAGAAGAGG GAAGGGGAGG GGAGGTGTCA GGGCGGTCGA GTCGGGAACC TCAAACGGGT
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FIG. 10C

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3101 GTTCCCCTTC CTGCTGCGTG GCCTCCAGAA GACTGCAGAC TTTGTGGAGG CCATCGAGGG GGCCCGGGCA GCATGCGCAG AGGCCGGCCA GGCTGGGGTG
     CAAGGGGAAG GACGACGCAC CGGAGGTCTT CTGACGTCTG AAACACCTCC GGTAGCTCCC CCGGGCCCGT CGTACGCGTC TCCGGCCGGT CCGACCCCAC

3201 CACGCCTACC CCAGCGGCTC CCCCTTCCTC TTCTGGGAAC AGTATCTGGG CCTGCGGCGC TGCTTCCTGC TGGCCGTCTG CATCCTGCTG GTGTGCACTT
     GTGCGGATGG GGTCGCCGAG GGGGAAGGAG AAGACCCTTG TCATAGACCC GGACGCCGCG ACGAAGGACG ACCGGCAGAC GTAGGACGAC CACACGTGAA

3301 TCCTCGTCTG TGCTCTGCTG CTCCTCAACC CCTGGACGGC TGGCCTCATA GTGAGTGCTT GCAGGAGTGG GGACAGAGAC ACCCCACCCT TCCCTGCCCA
     AGGAGCAGAC ACGAGACGAC GAGGAGTTGG GGACCTGCCG ACCGGAGTAT CACTCACGAA CGTCCTCACC CCTGTCTCTG TGGGGTGGGA AGGGACGGGT

3401 GCCTGTCATC CCTCCTGCCA GGAGCCCTCT GTGAGCCCTG TCTCCCTCAG GTGCTGGTCC TGGCGATGAT GACAGTGGAA CTCTTTGGTA TCATGGGTTT
     CGGACAGTAG GGAGGACGGT CCTCGGGAGA CACTCGGGAC AGAGGGAGTC CACGACCAGG ACCGCTACTA CTGTCACCTT GAGAAACCAT AGTACCCAAA

3501 CCTGGGCATC AAGCTGAGTG CCATCCCCGT GGTGATCCTT GTGGCCTCTG TAGGCATTGG CGTTGAGTTC ACAGTCCACG TGGCTCTGGT GAGCACGGGC
     GGACCCGTAG TTCGACTCAC GGTAGGGGCA CCACTAGGAA CACCGGAGAC ATCCGTAACC GCAACTCAAG TGTCAGGTGC ACCGAGACCA CTCGTGCCCG

3601 ACCCCGGGGA GGGACCAATC AGCTGATTCA GTATTCAACA CATATTGTTC AAGCCCCTAC TATGTGCTAG GTACTATTTA AGAATTTGGG CTGGGTGGAC
     TGGGGCCCCT CCCTGGTTAG TCGACTAAGT CATAAGTTGT GTATAACAAG TTCGGGGATG ATACACGATC CATGATAAAT TCTTAAACCC GACCCACCTG

3701 GTGGTGGCTC ATTCCTGTAA TCCCAGCACT TTGGGAGGCC GAGGCGGGTG GATCACCTGA GGTCGGGAGT TCGAAACCAG CCTGGCCAAC ATGGTGAAAC
     CACCACCGAG TAAGGACATT AGGGTCGTGA AACCCTCCGG CTCCGCCCAC CTAGTGGACT CCAGCCCTCA AGCTTTGGTC GGACCGGTTG TACCACTTTG

3801 CCTGTCTTTA CTAAAAATAC AAAAAATTAG CCAGGCGTGG TGGCACATGC CAGTAGTCCC AGCTACTTTG GAGGCTGAGG CAGAATTGCT TGAACCTGGG
     GGACAGAAAT GATTTTTATG TTTTTTAATC GGTCCGCACC ACCGTGTACG GTCATCAGGG TCGATGAAAC CTCCGACTCC GTCTTAACGA ACTTGGACCC

3901 AGGCGAAGGT TGCAGTGAGC TGAGATCGTG CCATTGCACT CCAGCCTGGG CAACAAGAGT GCAACTCTCC GTCTCAAAAA AAAAAAAAAA AAGGGCGGCC
     TCCGCTTCCA ACGTCACTCG ACTCTAGCAC GGTAACGTGA GGTCGGACCC GTTGTTCTCA CGTTGAGAGG CAGAGTTTTT TTTTTTTTTT TTCCCGCCGG

4001 GCGA
     CGCT
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FIG. 10D

Clone 16.1 human patched 2
> length: 2082 bp

> (SEQ ID NO:9)

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   1 TTCCGGCATG ACTCGATCGC CGCCCCTCAG AGAGCTGCCC CCGAGTTACA CACCCCCAGC TCGAACCGCA GCACCCCAGA TCCTAGCTGG GAGCCTGAAG
     AAGGCCGTAC TGAGCTAGCG GCGGGGAGTC TCTCGACGGG GGCTCAATGT GTGGGGGTCG AGCTTGGCGT CGTGGGGTCT AGGATCGACC CTCGGACTTC

 101 GCTCCACTCT GGCTTCGTGC TTACTTCCAG GGCCTGCTCT TCTCTCTGGG ATGCGGGATC CAGAGACATT GTGGCAAAGT GCTCTTTCTG GGACTGTTGG
     CGAGGTGAGA CCGAAGCACG AATGAAGGTC CCGGACGAGA AGAGAGACCC TACGCCCTAG GTCTCTGTAA CACCGTTTCA CGAGAAAGAC CCTGACAACC

 201 CCTTTGGGGC CCTGGCATTA GGTCTCCGCA TGGCCATTAT TGAGACAAAC TTGGAACAGC TCTGGGTAGA AGTGGGCAGC CGGGTGAGCC AGGAGCTGCA
     GGAAACCCCG GGACCGTAAT CCAGAGGCGT ACCGGTAATA ACTCTGTTTG AACCTTGTCG AGACCCATCT TCACCCGTCG GCCCACTCGG TCCTCGACGT

 301 TTACACCAAG GAGAAGCTGG GGGAGGAGGC TGCATACACC TCTCAGATGC TGATACAGAC CGCACGCCAG GAGGGAGAGA ACATCCTCAC ACCCGAAGCA
     AATGTGGTTC CTCTTCGACC CCCTCCTCCG ACGTATGTGG AGAGTCTACG ACTATGTCTG GCGTGCGGTC CTCCCTCTCT TGTAGGAGTG TGGGCTTCGT

 401 CTTGGCCTCC ACCTCCAGGC AGCCCTCACT GCCAGTAAAG TCCAAGTATC ACTCTATGGG AAGTCCTGGG ATTTGAACAA AATCTGCTAC AAGTCAGGAG
     GAACCGGAGG TGGAGGTCCG TCGGGAGTGA CGGTCATTTC AGGTTCATAG TGAGATACCC TTCAGGACCC TAAACTTGTT TTAGACGATG TTCAGTCCTC

 501 TTCCCCTTAT TGAAAATGGA ATGATTGAGT GGATGATTGA GAAGCTGTTT CCGTGCGTGA TCCTCACCCC CCTCGACTGC TTCTGGGAGG GAGCCAAACT
     AAGGGGAATA ACTTTTACCT TACTAACTCA CCTACTAACT CTTCGACAAA GGCACGCACT AGGAGTGGGG GGAGCTGACG AAGACCCTCC CTCGGTTTGA

 601 CCAAGGGGGC TCCGCCTACC TGCCCGGCCG CCCGGATATC CAGTGGACCA ACCTGGATCC AGAGCAGCTG CTGGAGGAGC TGGGTCCCTT TGCCTCCCTT
     GGTTCCCCCG AGGCGGATGG ACGGGCCGGC GGGCCTATAG GTCACCTGGT TGGACCTAGG TCTCGTCGAC GACCTCCTCG ACCCAGGGAA ACGGAGGGAA

 701 GAGGGCTTCC GGGAGCTGCT AGACAAGGCA CAGGTGGGCC AGGCCTACGT GGGGCGGCCC TGTCTGCACC CTGATGACCT CCACTGCCCA CCTAGTGCCC
     CTCCCGAAGG CCCTCGACGA TCTGTTCCGT GTCCACCCGG TCCGGATGCA CCCCGCCGGG ACAGACGTGG GACTACTGGA GGTGACGGGT GGATCACGGG

 801 CCAACCATCA CAGCAGGCAG GCTCCCAATG TGGCTCACGA GCTGAGTGGG GGCTGCCATG GCTTCTCCCA CAAATTCATG CACTGGCAGG AGGAATTGCT
     GGTTGGTAGT GTCGTCCGTC CGAGGGTTAC ACCGAGTGCT CGACTCACCC CCGACGGTAC CGAAGAGGGT GTTTAAGTAC GTGACCGTCC TCCTTAACGA

 901 GCTGGGAGGC ATGGCCAGAG ACCCCCAAGG AGAGCTGCTG AGGGCAGAGG CCCTGCAGAG CACCTTCTTG CTGATGAGTC CCCGCCAGCT GTACGAGCAT
     CGACCCTCCG TACCGGTCTC TGGGGGTTCC TCTCGACGAC TCCCGTCTCC GGGACGTCTC GTGGAAGAAC GACTACTCAG GGGCGGTCGA CATGCTCGTA
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FIG. 11A

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1001 TTCCGGGGTG ACTATCAGAC ACATGACATT GGCTGGAGTG AGGAGCAGGC CAGCACAGTG CTACAAGCCT GGCAGCGGCG CTTTGTGCAG CTGGCCCAGG
     AAGGCCCCAC TGATAGTCTG TGTACTGTAA CCGACCTCAC TCCTCGTCCG GTCGTGTCAC GATGTTCGGA CCGTCGCCGC GAAACACGTC GACCGGGTCC

1101 AGGCCCTGCC TGAGAACGCT TCCCAGCAGA TCCATGCCTT CTCCTCCACC ACCCTGGATA ACATCCTGCA TGCGTTCTCT GAAGTCAGTG CTGCCCGTGT
     TCCGGGACGG ACTCTTGCGA AGGGTCGTCT AGGTACGGAA GAGGAGGTGG TGGGACCTAT TGTAGGACGT ACGCAAGAGA CTTCAGTCAC GACGGGCACA

1201 GGTGGGAGGC TATCTGCTCA TGCTGGCCTA TGCCTGTGTG ACCATGCTGC GGTGGGACTG CGCCCAGTCC CAGGGTTCCG TGGGCCTTGC CGGGGTACTG
     CCACCCTCCG ATAGACGAGT ACGACCGGAT ACGGACACAC TGGTACGACG CCACCCTGAC GCGGGTCAGG GTCCCAAGGC ACCCGGAACG GCCCCATGAC

1301 CTGGTGGCCC TGGCGGTGGC CTCAGGCCTT GGGCTCTGTG CCCTGCTCGG CATCACCTTC AATGCTGCCA CTACCCAGGT GCTGCCCTTC TTGGCTCTGG
     GACCACCGGG ACCGCCACCG GAGTCCGGAA CCCGAGACAC GGGACGAGCC GTAGTGGAAG TTACGACGGT GATGGGTCCA CGACGGGAAG AACCGAGACC

1401 GAATCGGCGT GGATGACGTA TTCCTGCTGG CGCATGCCTT CACAGAGGCT CTGCCTGGCA CCCCTCTCCA GGAGCGCATG GGCGAGTGTC TGCAGCGCAC
     CTTAGCCGCA CCTACTGCAT AAGGACGACC GCGTACGGAA GTGTCTCCGA GACGGACCGT GGGGAGAGGT CCTCGCGTAC CCGCTCACAG ACGTCGCGTG

1501 GGGCACCAGT GTCGTACTCA CATCCATCAA CAACATGGCC GCCTTCCTCA TGGCTGCCCT CGTTCCCATC CCTGCGCTGC GAGCCTTCTC CTTACAGCCA
     CCCGTGGTCA CAGCATGAGT GTAGGTAGTT GTTGTACCGG CGGAAGGAGT ACCGACGGGA GCAAGGGTAG GGACGCGACG CTCGGAAGAG GAATGTCGGT

1601 TCCTCAGCCT GGACCTACGG CGGCGCCACT GCCAGCGCCT TGATGTGCTC TGCTGCTTCT CCAGTCCCTG CTCTGCTCAG GTGATTCAGA TCCTGCCCCA
     AGGAGTCGGA CCTGGATGCC GCCGCGGTGA CGGTCGCGGA ACTACACGAG ACGACGAAGA GGTCAGGGAC GAGACGAGTC CACTAAGTCT AGGACGGGGT

1701 GGAGCTGGGG GACGGGACAG TACCAGTGGG CATTGCCCAC CTCACTGCCA CAGTTCAAGC CTTTACCCAC TGTGAAGCCA GCAGCCAGCA TGTGGTCACC
     CCTCGACCCC CTGCCCTGTC ATGGTCACCC GTAACGGGTG GAGTGACGGT GTCAAGTTCG GAAATGGGTG ACACTTCGGT CGTCGGTCGT ACACCAGTGG

1801 ATCCTGCCTC CCCAAGCCCA CCTGGTGCCC CCACCTTCTG ACCCACTGGG CTCTGAGCTC TTCAGCCCTG GAGGGTCCAC ACGGGACCTT CTAGGCCAGG
     TAGGACGGAG GGGTTCGGGT GGACCACGGG GGTGGAAGAC TGGGTGACCC GAGACTCGAG AAGTCGGGAC CTCCCAGGTG TGCCCTGGAA GATCCGGTCC

1901 AGGAGGAGAC AAGGCAGAAG GCAGCCTGCA AGTCCCTGCC CTGTGCCCGC TGGAATCTTG CCCATTTCGC CCCGGAATTC CTGCAGCCCG GGGGATCCAC
     TCCTCCTCTG TTCCGTCTTC CGTCGGACGT TCAGGGACGG GACACGGGCG ACCTTAGAAC GGGTAAAGCG GGGCCTTAAG GACGTCGGGC CCCCTAGGTG

2001 TAGTTCTAGA GCGGCCGCCA CCGCGGTGGA GCTCCAGCTT TTGTTCCCTT TAGTGAGGGT TAATTGCGCG CTTGGGTATC TT
     ATCAAGATCT CGCCGGCGGT GGCGCCACCT CGAGGTCGAA AACAAGGGAA ATCACTCCCA ATTAACGCGC GAACCCATAG AA
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FIG. 11B